

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

Human 33312

Cytochrome p450 Domain

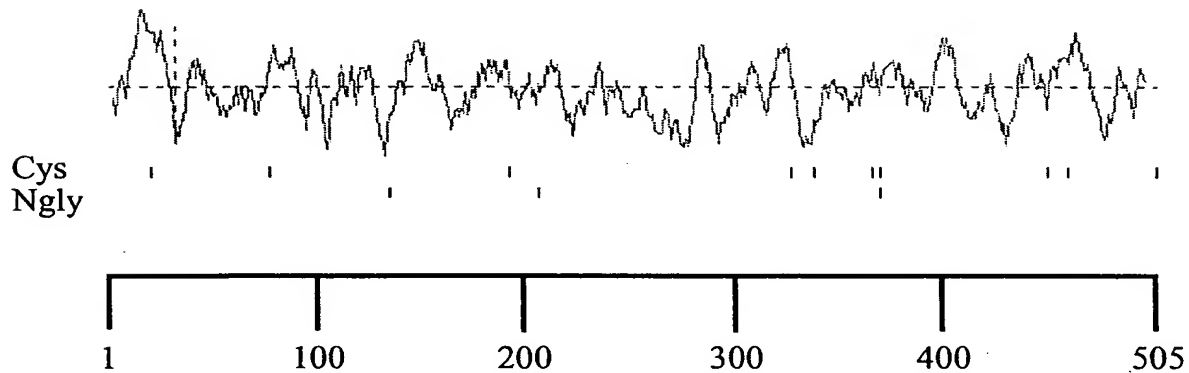


Fig. 1

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p450: domain 1 of 1, from 46 to 501: score 400.9, E = 1.2e-116:

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*->PPGPpplliGnllqlgrapppiphsltklrkakrYgkpvftlylGp
  +P Pp +++ G+ +++ ++ +++++kl + k Y+ ++l++Gp
33312 46 FPAPPAHWFYGHKEFYPV--KEF-EVYHKLME-K-YP-CAVPLWVGP 86

      .rpvVltgpeavkevLidkgeeFakgRgdfnptfpwlsgyreggllfs
      + +++++p+++ +L ++ + ++ + + + w+ g gl+++
33312 87 fTMFFSVHDPDYA-KILLKRQDPKS-AVSHK-ILESWV--GR---GLVTL 128

      dnGpkWrklRrFslltlrfHFgmGa....ysKrsqkleePriqeeardLv
      +G kW+k+R+ + + F + + ++ ++ ++ + + ++
33312 129 -DGSKWKKHRQ--IVKP-G-FNI-SilkiFI-T---MMS-ESVRMMLNKW 167

      erlrkeqagspiDitellarlaplnvicsllF...Gvrfdylrpedpef
      e+ + q +s ++++++++ l++l+ I++++F+++++++d+ D+ +
33312 168 EEHIA-Q-NSRLELFQHS-LMTLDSIMKCAFshqgsIQlds--TLDS-Y 211

      lkldkl1nemfdrvspwhqlldifp...fllrylpgs1frkafkaakd.
      lk++ + l +++ + ++ +++ +++ +++ s + ++f ++ +
33312 212 LKAVERN-LSKIS-N-Q---RMNNFLHndLVFKF--SS-QGQIFSKFNQe 252

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Fig. 2A

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lkdyldklierretlepagdpRrLD.i.....gfldslleakreggnp
l+++++k+i++r+e+l+ + D++++++ +fld+ Ll ak e+
33312 253 LHQFTEKVIQDRKESLKD-KLKQ--DtTqkrrwDFLDI-LLSAKSENT-- 296

kselSdeelaatvldllfAGteTTsstLswaLyLlakhPevqaklreEid
+ +s+ +l a+v +++fAG++TTss++sw+Ly Lak+Pe+q+++r Ei
33312 297 -KDFSEADLQAEVKTFMFAGHDTTSSAISWILYCLAKYPEHQRCRDEIR 345

eviGrdrsptydvDaraqmPYLdAvIkEtLRlypvvPl1lprvatkDtei
e +G+++s+t++ + ++qmpY++++Ike LRly +v ++ R + k++++
33312 346 ELLGDGSSITWE-H-LSQMPYTTMCIKECLRLYAPV-VNISRLLDKPITF 392

pdGylIPKGtlVivnlyslhrDpkvfpnPeeFdPeRFLdengkfksyaf
pdG+ +P+G +V++n++++lh++p +++++P++F+P RF+ en + ++yaf
33312 393 PDGRSLPAGITVFINIWAHHPYFWEDPQVFNPLRFSRESENSEKIHPYAF 442

lPFGaGpRnClGerlArmElflflatlLqrFPelelelavppgdipsltpkp
+PF+aG RnC+G+++A+ E +++++a+ L rF +l +++++ +p +p +
33312 443 IPFSAGLRNCIGQHFAIIECKVAVALTLRF-KLA--PDHSRPP--QPVR 487

elglpskpplykvqlrpa<-* (SEQ ID NO:10)
+++l sk++++ + a
33312 488 QVVLKSKNGIH---VF-A 501

```

Fig. 2B

Applicant: Rachel E. Meyers, et al.

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THEREOF

Attorney/Agent: Janice M. Klunder

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Human 33303

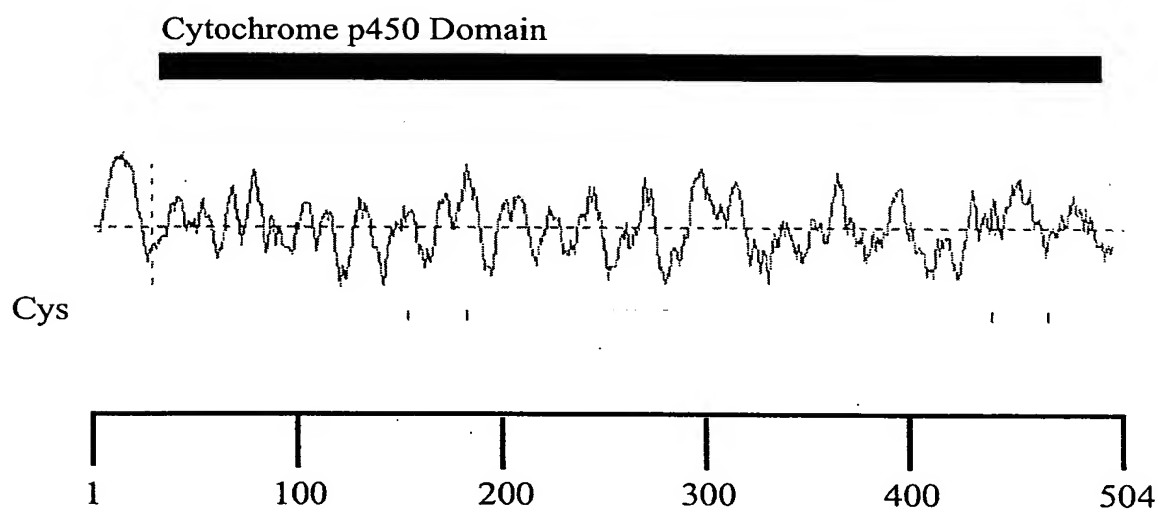


Fig. 3

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p450: domain 1 of 1, from 33 to 493: score 594.5, E = 6.4e-175:

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*->PPgPpplPliGnllqlgrappiph.sltklrkakyGkpvftlylG
  PPGP+plPl+Gnllql+  g + ++ l++l+k k YG pvft+yYG
33303 33  PPGPTPLLLGNLLQLRP--GAL-YsGLMRLSK-K-YG-PVFTIYLG 73

  p.rpvVvltgpeavkevLldkgeeFakGRgdfnptfpwlsgkyregllf
  p.rpvVv1 g eav+e+l+ +eeF+ gRG ++++ ++g+ g++f
33303 74 PwRPVVVLVGQEAVREALGGQAEFFS-GRGTV-AMLEGTFDGH---GVFF 118

  sdnGpkWrklRrFs11tlrHFgmGaysKrsqkleePriqeeardLverl
  s nG++Wr+lR+F++l+l+r+ +gmG Kr ee iq ear+Lve++
33303 119 S-NGERWRQLRKFTMLALRD-LGMG---KRE--GEE-LIQAEARCLVETF 160

  rkegagspiDitellarlaplInvicsllFGvrfdylrpeDpeflklidkl
  + + g p+D++ 1la a++nv+csllFG rf Y eD+ef++ ++ +
33303 161 QGTE-GRPFDPsLLLA-QATSNVVCsLLfGLRFSY---EDKEFQAVVR-A 204

  lnemfdrvspwh.qlldiFP.fLlrylpgs1frkafkaakdkldkldli
  +++ vs+ ++q + +f fL++ lpg+ +++++ + 1 +++++ +
33303 205 AGGTLIGVSSQGgQTYEMFSwFLRP-LPGP-HKQLLHHVSTLAAFTVRQV 252

```

Fig. 4A

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eerretlepagdpRrldigfldsllleakreggnpkselsdeelaatvld
+++ l+ g+ R D ++D++Ll++ ++ np ++++++ ++tv+
33303 253 QQHQNLDASGPARG--D--LVDAFLLKMAQEEQNPGTEFTNKNMLMTVIY 298

llfAGteTtsstlswaLyllLakhPevqaklreEideviGrdrsptydvdA
llfAGt T+s+t ++L+ll+k+p+vq+ +reE+ + +G ++ p++ D
33303 299 LLFAGTMTVSTTVGYTLLLLMKYPHVQKWVREELNRELGAGQAPSLG-D- 346

raqmPYLdAvIkEtLRlypvvPlllprvatkDteiPdGylIPKGtlVivn
r ++PY+dAv++E++Rl +vP+++pR++ + t + +Gy++P Gt V++
33303 347 RTRLPYTDAVLHEAQRLLALVPMGIPRTLMTTRF-RGYTL PQGTEVFPL 395

lyslhrDpkvfpnPeeFdPeRFLdengkfksyafLPFGaGpRnClGerl
l+s+++Dp+++f +PeeF+P+RFLd++g+f+k++afLPF+ G+R+ClGe+l
33303 396 LGSILHDPNIFKHPEEFNPDRLDADGRFRKHEAFLPFSLGKRVCLGEGl 445

ArmElflflatlLqrFPelelavppgdipsltpkpelglpskpplykvql
A+ Elflf++t+Lq F +le+++pp + l+p + +gl ++pp + ql
33303 446 AKAEFLFFTTILQAF-SLESPCPPDTLS-LKPTV-SGLFNIPPAF--QL 490

rpa<-* (SEQ ID NO:10)
++
33303 491 QVR 493

```

Fig. 4B

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THEREOF

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Human 32579

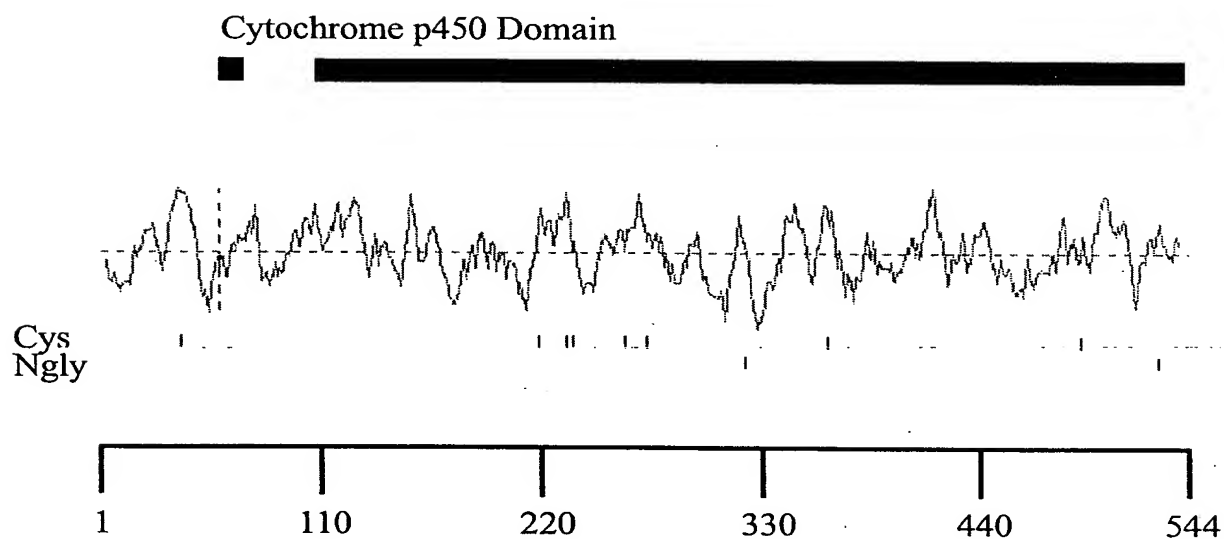


Fig. 5

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p450: domain 1 of 2, from 60 to 72: score 7.8, E = 0.21:

->PPgPpplPliGnl<- (SEQ ID NO:11)

PPgP+p+Pl+Gn+
32579 60 PPGTPWPLVGNF 72

Fig. 6A

p450: domain 2 of 2, from 107 to 543: score 516.2, E = 2.3e-151:

*->ltklrkakrYGkpvftlylGprpvVltgpeavkevLldkgeefakg
1+ 1++ YG ++f++ +G+ vVvl++ v+e+L++++e F+ +
32579 107 LAHLAR-V-YG-SIFSFFIGHYLVVLSDFHSVREALVQQA EVFS-D 149

RgdfnptfpwlskgyreqgllfsdnGpkWrklRrFslltlrfHFgmGays
R++ p +++k + g++f+ +Gp+W++R+Fs+ tlr Fg+G
32579 150 RPRV-PLISIVTKEK---GVVFAHYGPVWRQQRKFSTLRH-FGLG--- 191

KrsqkleePriqeeardLverlrkeqagspiDitellarlaplnvicsll
K+s le p i ee + ++k++ p+ ++ ++ a++n+Icsl+
32579 192 KLS--LE-PKIIIEEFKYVKAEMQKHG-EDPFCPFSIIS-NAVSNIICSLC 236

FGvrfdylrpeDpeflklidklldnemfdrv.spwh.qlldiffPllryl.
FG rfdy ++ef k++ ++ + ++ + l++i P+L +Yl+
32579 237 FGQRFDY---TNSEFFKMLG-FMSRGL-EICLNSQVLLVNICPWL-YYLp 280

Fig. 6B

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pgslfrkafkaakd.lkdylldklieerretlepagdpRrldigfldslLl
g+ f+++ ++++++ +l k+i+++++e+l++ +p D f+D Ll
32579 281 FGP-FKELR-QIEKdITSFLKKIiKDHQESLDR-ENPQ--D--FIDMYLL 323

eakr.eggnpkxselsdeelaatvldllfAGteTtsstLswaLyLlakhPe
+++++++n +s+++++e l +++dl+++AGt+TT++ L w+L+++ +P+
32579 324 HMEERKNNSNSSFDEEYLYFYIIGDLFIAGTDTTNSLLWCLLYMSLNPD 373

vqaklreEideviGrdrsptydvDaragmPYLdAvIkEtLRlypvvPlll
vq+k++eEi+++viG +r p++ D aqmpY++A+I E++Rl vvPl++
32579 374 VQEKVHEEIERVIGANRAPSLT-D-KAQMPTYTEATIMEVQRLTVVPLAI 421

prvatkDteiPdGylIPKGtlVivnlyslhrDpkvfpnPeeFdPeRFLde
p+++++ t++ +Gy+IPKGtl+++nl+s+hrDp+++++Pe F P RFLd
32579 422 PHMTSENTVL-QGYTIPKGTLILPNLWSVHRDPAIWEKPEDFYPNRFLDD 470

ngkfksyaflPFGaGpRnClGerlArmeIfLfLatllqrFPeleleavpp
+g+ k + f+PFG G+R+C Ge+lA+mElfl++ +l+q F + l+ +
32579 471 QGQLIKKETFIPIFGIGKRVCVMGEQLAKMEFLMFVSLMQSF-AFALPEDS 519

gdipsltpkpelglskpplykvqlrpa<-* (SEQ ID NO:12)
+++ lt++ +gl++ p ++++++ +
32579 520 KKPL-LTGR--FGLTLAPHFNITIS-R 543

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Fig. 6C

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Attorney/Agent: Janice M. Klunder

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CCCACGGTCCGCCAGAGTGGGCGCAGGAGGTGTCGGTGCCGAGCGGGGTTTTTTTTTCTGCGGGTTGCCTTTTGT

TTTTCTTTGGAACCGCGGTTGTTCAAAAGCTTGACGGAACCTTGAAGGGGACTCCCACTCTCCTCCCTCTTTCCGCTG

M D K V C A I F G G S R G I G	15
AGTTTGTGACTCCGAG ATG GAC AAA GTG TGT GCT ATT TTT GGA GGC TCC CGA GGC ATT GGC	45
R A V A Q L M A R K G Y R L A I I A R N	35
AGG GCT GTG GCC CAG TTA ATG GCC CGG AAA GGC TAC CGC CTG GCG ATC ATT GCC AGA AAC	105
L E G A K A A A G D L G G D H L A F S C	55
CTG GAA GGG GGC AAA GCC GCC GCC GGT GAC CTC GGC GGA GAT CAT TTG GCA TTT AGC TGT	165
D V A K E H D V Q N T F E E M E K H L G	75
GAT GTT GCT AAA GAA CAT GAT GTT CAA AAT ACA TTT GAA GAG ATG GAG AAA CAT TTA GGT	225
R V N F L V N A A G I N R D S L L V R T	95
CGA GTA AAT TTC TTG GTA AAT GCA GCT GGT ATT AAC AGG GAT AGT CTT TTA GTA AGA ACA	285
K T E D M V S Q L H T N L L G S M L T C	115
AAA ACT GAA GAT ATG GTA TCT CAG CTT CAT ACT AAC CTC TTG GGT TCC ATG CTG ACC TGT	345
K A A M R A M I Q Q Q G G S I V N V G S	135
AAA GCT GCC ATG AGG GCT ATG ATT CAA CAA CAG GGA GGG TCT ATT GTT AAT GTA GGA AGC	405
I V G L K G N S G Q S V Y S A S K G G L	155
ATT GTT GGC TTA AAA GGC AAC TCT GGC CAG TCC GTT TAC AGT GCC AGT AAA GGA GGA TTA	465
V G F S R A L A K E V A R K K I R V N V	175
GTT GGA TTT TCA CGT GCT CTT GCT AAA GAG GTA GCA AGA AAG AAA ATT AGA GTG AAT GTA	525
V A P G F V H T D M T K D L K E E H L K	195
GTT GCA CCA GGA TTT GTA CAC ACA GAT ATG ACG AAA GAC TTG AAA GAA GAA CAT TTA AAG	585
K N I P L G R F G E T I E V A H A V V F	215
AAA AAT ATT CCT CTT GGG AGG TTT GGA GAA ACT ATT GAG GTG GCA CAT GCG GTT GTG TTT	645
L L E S P Y I T G H V L V V D G G L Q L	235
CTT TTA GAA TCA CCG TAT ATT ACA GGG CAT GTT CTG GTA GTG GAT GGG GGA TTA CAA CTC	705
I L	238
ATT TTG TAA	714

TTTGACAGATTATTCAAGTTATAGGGGTGATTAGCATCAAGGGCACACTTTGGCTACTGATTAGACAATTATACCTACATG
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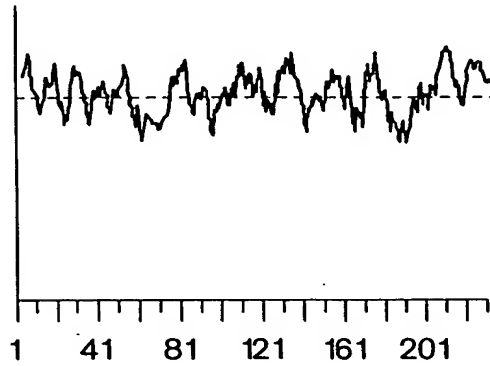
Fig. 7

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THEREOF

Attorney/Agent: Janice M. Klunder

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>21509

MDKVCAIFGGSRGIGRAVAQLMARKGYRLAI IARNLEGAKAAAGDLGGDHLAFSCDVAKE
HDVQNTIFEEMEKHLGRVNFVNAAGINRDSLLVRTKTEDMVSQ LHTNLLGSMLTCKAAMR
AMIQQQGGSI VNVGSIVGLKGNSSQSVYSASKGGLVGF SRALAKEVARKKIRVNVVAPGF
VHTDMTKDLKEEHLKKNIP LGRFGETIEVAHAVVFLLSPYITGHVLVVDGGLQLIL

Fig. 8

adh_short: domain 1 of 1, from 3 to 184: score 217.5, E = 2e-61

```

      *->KvaLvTGassGIGlaiAkrLakeGakVvvadrneeklekGavakelk
      Kv+ + G+s+GIG+a+A+ +a++G+++++rn e +      +++
21509   3      KVCAIFGSGRGIGRAVAQLMARKGYRLAI IARNLEGA-----KAAAG 44

      elGgndkdralaiqlDvtdeesv.aaveqaverlGrlDvLVNNAGgiill
      lGg      la+ +Dv++e +v++++e+ ++lGr++ LVN AG i
21509  45  DLGG----DHLAFSCDVAKEHDVqNTFEEMEKHLGRVNFVNAAAG--I-N 87

      rpgpfaelstneedwdrvidvNltgvfilltravplmamkkrggGrIvN
      r+ + +      ed + +++Nl+g +l+++a+++ am++++gG+IvN
21509  88  RDSLLVVRTK---TEDMVSQLHTNLLGSMLTCKAAMR--AMIQOQGGGIVN 132

      iSSvaGrkegglvgcpggsaYsASKaAvigltrsLAlElaphgIrVnava
      ++S++G      l+g+ g+s+YsASK++++g++r+LA+E+a+++IrVn+va
21509 133  VGSIVG-----LKGNSGQSVYSASKGGLVGFSRALAKEVARKKIRVNVVA 177

      PGgvdTd<-*
      PG+v Td
21509 178  PGFVHTD      184

```

Fig. 9A

adh_short_C2: domain 1 of 1, from 201 to 229: score 29.6, E = 1.1e-06

```

      *->gRlGePeEiAnavvFLASdaAsYiTGqtlvV<-*
      gR+Ge+ E+A avvFL  ++ YiTG++lvV
21509 201  GRFGETIEVAHAVVFL--ESFYITGHVLV  229

```

Fig. 9B

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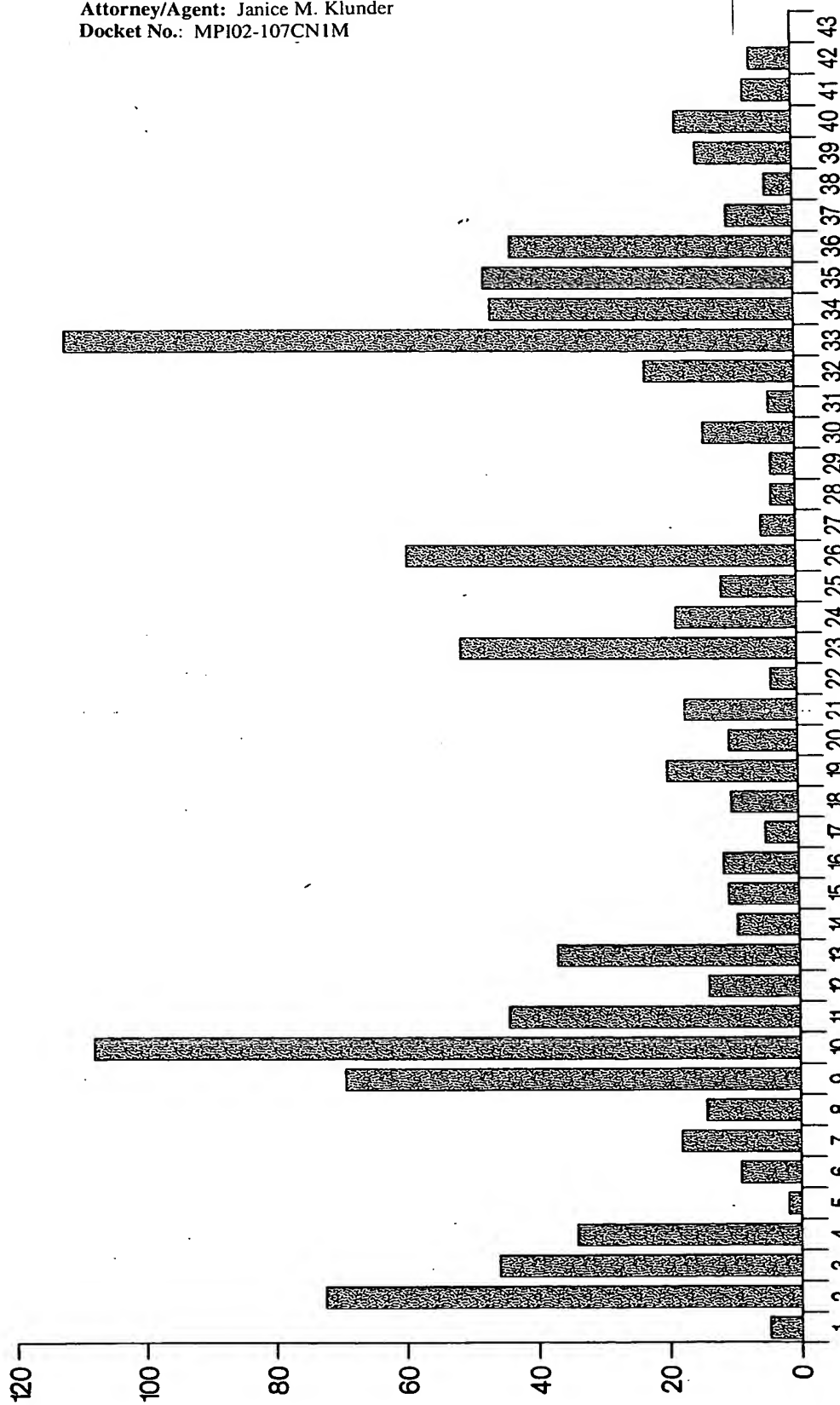


Fig. 10

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

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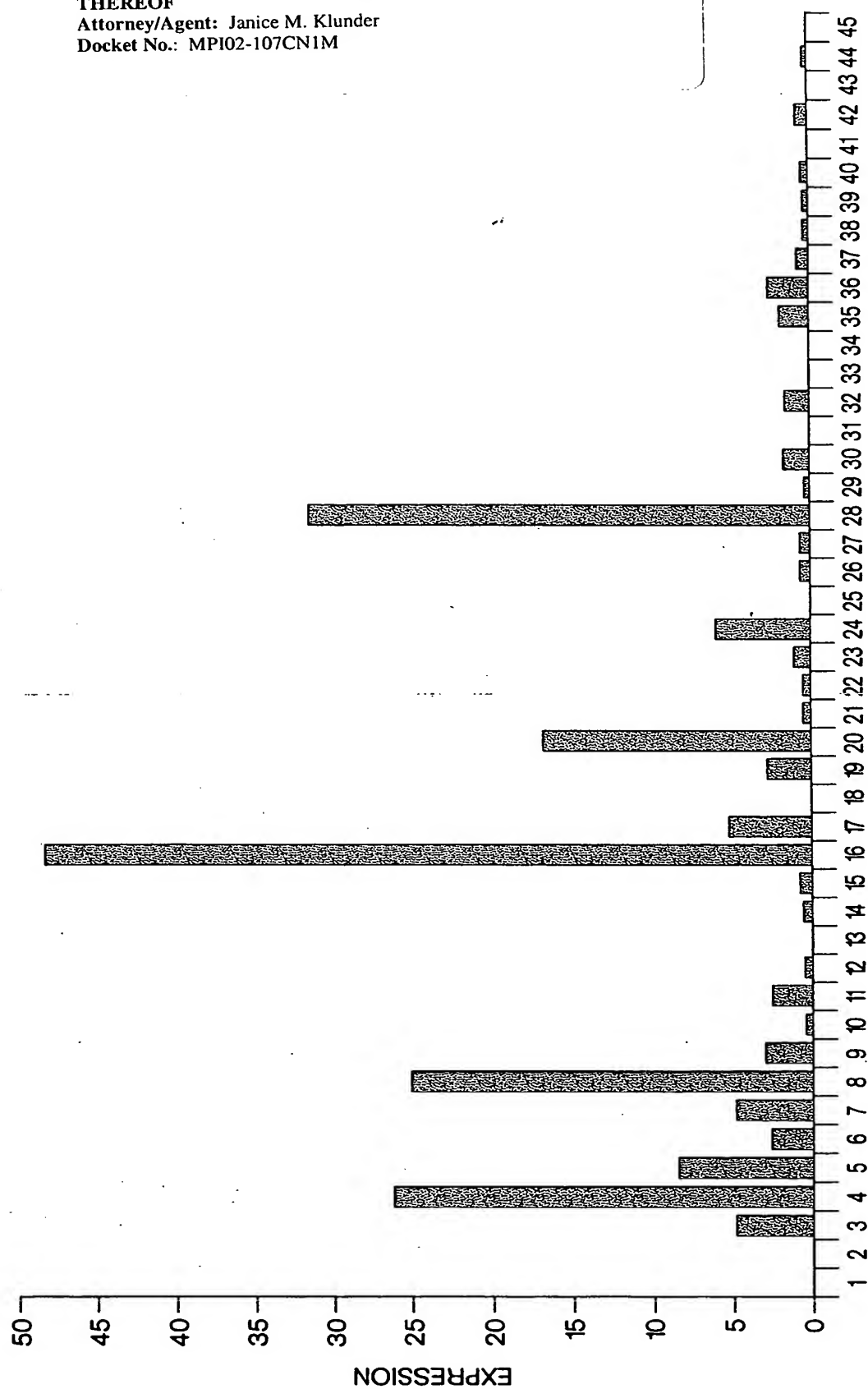


Fig. 11

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Docket No.: MPI02-107CN1M

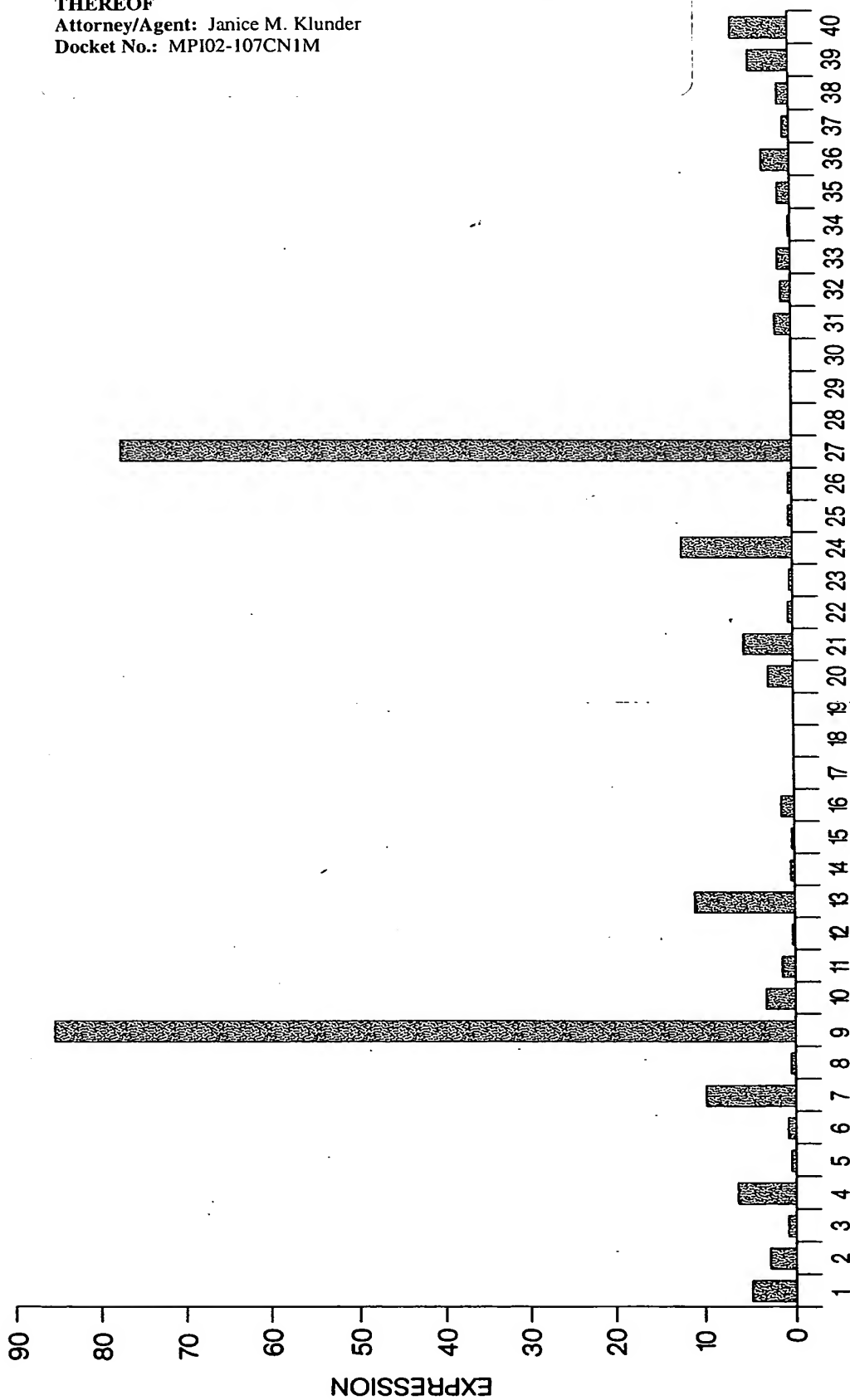


Fig. 12

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Q I W C G E G V D K L S L P A R N Q A G 370
 CAA ATT TGG TGC GGT GAG GGA GTG GAT AAG TTG AGC CTC CCT GCC AGG AAC CAG GCA GGC 1110

 Y F M L P T V I T D I K D E S C C M T E 390
 TAC TTT ATG CTT CCC ACG GTG ATA ACA GAC ATT AAG GAT GAA TCC TGC TGC ATG ACG GAA 1170

 E I F G P V T C V V P F D S E E E V I E 410
 GAG ATA TTT GGT CCA GTG ACG TGT GTC GTC CCC TTT GAT AGT GAA GAG GAG GTG ATT GAA 1230

 R A N N V K Y G L G A T V W S S N V G R 430
 AGA GCC AAC AAC GTT AAG TAT GGG CTG GGG GCT ACC GTG TGG TCC AGC AAT GTG GGG CGC 1290

 V H R V A K K L Q S G L V W T N C W L I 450
 GTC CAC CGG GTG GCT AAG AAG CTG CAG TCT GGC TTG GTC TGG ACC AAC TGC TGG CTC ATC 1350

 R E L N L P F G G M K S S G I G R E G A 470
 AGG GAG CTG AAC CTT CCT TTC GGG GGG ATG AAG AGT TCT GGA ATA GGT AGA GAG GGA GCC 1410

 K D S Y D F F T E I K T I T V K H * 488
 AAG GAC TCT TAC GAC TTC TTC ACT GAG ATC AAA ACC ATC ACC GTT AAA CAC TGA 1464

 TCTTTGCTAATGGTGGAGCCACTATGGCCAATGCCTGGCTGCAGGCATCAGTTGTTCAATGTGGTAGATGAAAATCATG
 GCATGAATTCCAGCTATGCCTTGACTTGGCAGAAGGTTATCTCTAGCTTATCCTCAGTTCTTAGTAACCTTTACCCACTA
 GTGAAGAGATACTGTCTATTTTCAATGTGGACTCGGAAAAAAGACTTATAAGTAGGAAGATAGAACAATGATGCCAGT
 TGTCAGGCTCCTCCCAGGTTATGTTTTCATAGTGTTCCTTTCATCATCTTCATTGAACTCTTGGGAATCTCCAGATAAT
 CAGATTATTTTCAATTTGGTAAATTTTAAAAAATATGCAATCAGGCACAGTGCCTCATGCCTATAATCCCAGCACTTTGGG
 AGGCCAAGGTGGGTGGATCACTTGAGTTCAGGAGTTCGAGATCAGCCTAGGCAACATGGTGAAATCCTGTCTTTACCAA
 AAGTTTAAAAATTAGCTTGGTGTGGTGCCCTCTGCCTATAGCCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATCGCTT
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 TTTAAAAA

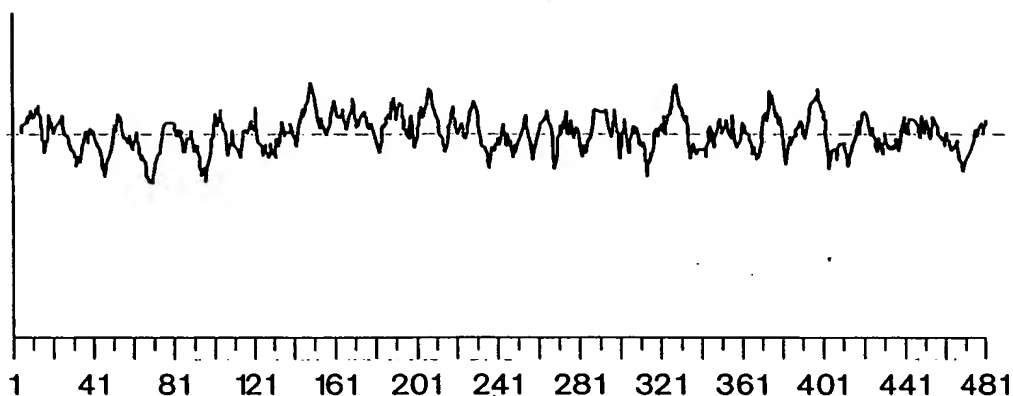
Fig. 14B

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>33770

MAGTNTLLMLENFIDGKFLPCSSYIDSYDPSTGEVYCRVPNSGKDEIEAAVKAAREAFPS
WSSRSPQERSRVLNQVADLLEQSLEEFQAESKDQGKTLALARTMDIPRSVQNFRFFASS
SLHHTSECTQMDHLGCMHYTVRAPVGVAGLISPWNLPYLLTWKIAPAMAAGNTVIKPS
ELTSVTAWMLCKLLDKAGVPPGVVNIVFGTGPRVGEALVSHPEVPLISFTGSQPTAERIT
QLSAPHCKKLSLELGGKNPAIIFEDANLDECIPATVRSSFANQGEICLCTSRIFVQKSIY
SEFLKRFVEATRKKVGI PSDPLVSIGALISKAHLEKVR SYVKRR LAEGAQIWC GEGVDK
LSLPARNQAGYFMLPTVITDIKDESCMTEEI FG PVT CVVPFDSEEEVIERANNV KYGLG
ATVWSSNVGRVHRVAKKLQSGLVWTNCWLI REINLPFGGMKSSGIGREGAKDSYDFFTEI
KTITVKH

Fig. 15

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Alignments of top-scoring domains:

alddedh: domain 1 of 1, from 17 to 487: score 656.6, E = 1.3e-193

```

      *->ewvdsasgkttfevvnPankgevigrvpeataeDvdaAVkAAkeAfks
      ++ +      ++++++P++ gev +rvp+++++++aAVkAA+eAf+s
33770   17   KFLPC--SSYIDSYDPST-GEVYCRVPNSGKDEIEAAVKAAREAFPS 60

      GpwWakvpaseRariLrkladlieeredelaaletlDlGKplaeAkGdte
      wt +tt eR+r+L++ adl+et ++e+a +ettD+GK+la A ++
33770   61   ---WSSRSPQERSRVLNQVADLLEQSLEEFQAESKDQGKTLALART-MD 106

      vgraideiryyagwarklmgerrvipslatdgdeelnnytrrePlGVvgvI
      ++r +++++r++a      + +tt ++ ++ +      + yt+r P+GV g I
33770  107   IPRSVQNFRRFFASSSL--HHTSECTQMDHLG---CMHYTVRAPVGAGLI 151

      sPWNFPlllalwklapALAAgNTVVlKPSEqTPltalillaelieeaGann
      sPWN Pl l++wk+apA+AAgNTV+ KPSE+T +ta l++l+++aG
33770  152   SPWNLPlyLLTWKIAPAMAAGNTVIAKPSELTSVTAWMLCKLLDKAG--- 198

      lPkGVvnvvpGfGaevGqaLkshpdlidlisFTGSteVGklimeaAAaknl
      +P+GVvn+V G G+ vG aL+shp + isFTGS+++ + i +      a +
33770  199   VPPGVVNIVFGTGRVGEALVSHPEVPLISFTGSQPTAERITQ-LSAPHC 247

      kkVtLELGGSsPvIVfdDADLdkAverivfgaFgnaGQvCiApsRllVhe
      kk +LELGGS+P I+f+DA+Ld ++ ++v++ F n+G++C ++sR++V++
33770  248   KKLSLELGGSNPAIIFEDANLDECIPATVRSSFANQGEICLCTSRIFVQK 297

      siydeFveklkervkkkliGdpldsdtniyGPlIseqqfdrvlslYedg
      siy eF+++ +ett k+k +G p dt ++i G+lIs++++++v sy++++
33770  298   SIYSEFLKRFVEATRKKW-VGIPSDPLVSI-GALISKAHLEKVRSYVKRA 345

      keeGakvlcG.Gerdeskeylgg.GyyvqPTiftDVtpdMkImkEEIFGP
      +eGA++ cG+G      s++ ++ Gy+ PT++td+++++ +m EEIFGP
33770  346   LAEGAQIWCGeGVDKLSLPARNQaGYFMLPTVITDIKDESCCMTEEIFGP 395

      VlpiikfkdldeAIelaNdtEYGLAayvFTkdilarafrvakaleaGiVw
      V +++ f++++E+Ie+aN+++YGL+a v++++ r++rvak+l++G Vw
33770  396   VTCVVPFDSEEEVIERANNVYGLGATVWSSN-VGRVHRVAKKLQSGLVW 444

      vNDvcvhaaepqlPFGGvKqSSGiGrehgGkygleeYteiKtVtirl<-*
      N c+ + e +lPFGG+K SGiGret k++ +++teiKt+t+++
33770  445   TN--CWLIRELNLPFGGMKS-SGIGREG-AKDSYDFFTEIKTITVKH 487

```

Fig. 16

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

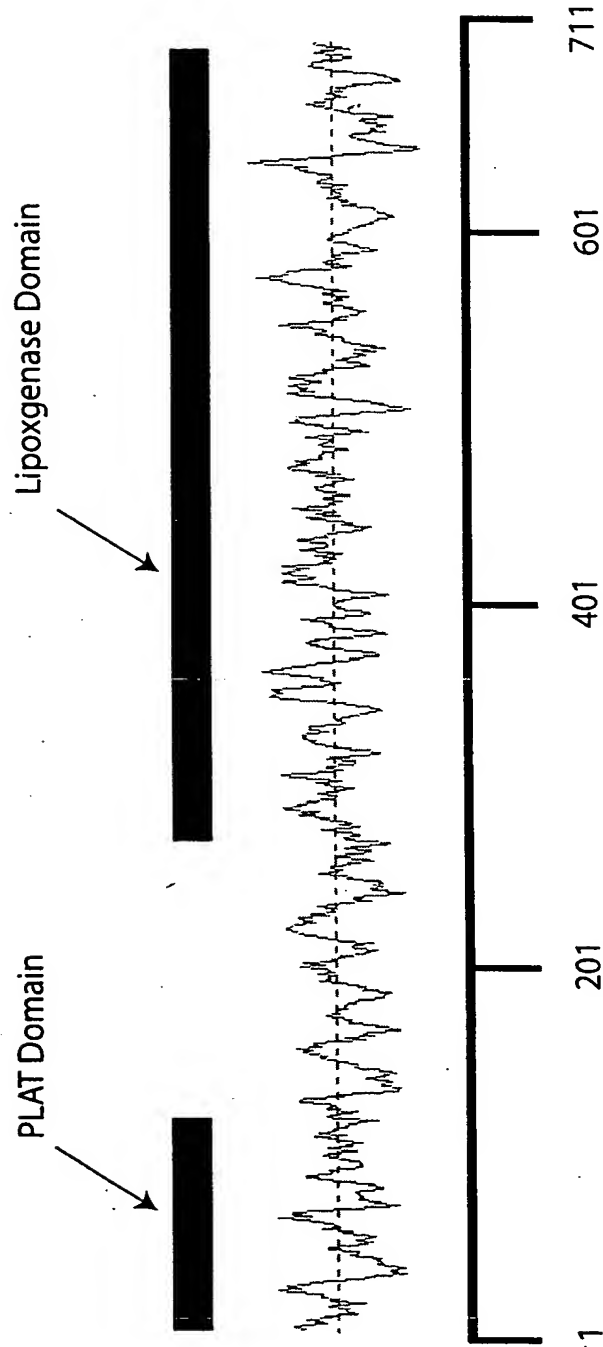


Fig. 17

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

lipoxxygenase: domain 1 of 1, from 267-703: score 480.2, E=1.7e-140

```

*->aWmtDeeFAREmLAGvNPvvIrrlqeFPpkSKLDpavYGDqtStITk
      +W +D +F+++ L+GvNPv++ ++ ++P+k          +++T
46638 267   HWCEDHFFGYQYLYNGVNPVMLHCISLPSK-----LPVTN 301

      ehLElnL.gglTVeeAlqngrLFilDhhDlfiPylnkInsItstklYAtR
      +++ + L+  ++ +l+ g++F +D+ l  + n  +++ +A++
46638 302 DMVAPLLgQDTClQTELErGNIFLADYWILAEAPThCLN-GRQQYVAAPL 350

      TlFLkDgtLkPlAieLslPhpdgdpfGavskVflPadeGvessiWLLA
      +lL L++ g L+PlAI+Ls + p+ d  s++flP+d  ++WLLA
46638 351 CLLWLSPOGALVPLAIQLS-QTPGPD-----SPIFLPTDS---EWDWLLA 391

      KayVrvnDsgyHQLiSHWLnTHavvEPFvIATnRqLSvlHPiYKLLlPHY
      K++Vr++ + +H+  +H L TH+  E F+ AT RqL+  HPiYKLLlPH
46638 392 KTWVRNSEFLVHENNTFLCTHLLCEAFAMATLRQLPLCHPIYKLLlPHT 441

      RdTMnINaLArqsLinagIiEktflpgkyGaveMssavykKdWvFtdqA
      R+T+  N+ AR +L n +G+ ++  + g+ G + + s  + + ++t ++
46638 442 RYTLQVNTIARATLLNPEGLVDQVTSIGRQGLIYLMSTGLA-HFTYTNFC 490

      LPaDLvkRGlaveDpssPhGvRllIedYPYAvDGLeiWdaIktWVqeyVs
      LP+ L +RG++          I+ Y Y++DGL iW+aI+++V e+v
46638 491 LPDSLRRARGVLA-----IPNYHYRDDGLKIWAAlESFVSEIVG 528

```

Fig. 18A

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

```

LYYksDeavkkDpELQaWWkEvrevGHGdkKDepWWpklqtredLievCT
YY+sD++v++D+ELQaW E+ ++ +++++ 1 t+ + ++++T
46638 529 YYYPsDASVQDSELQaWTGEIFAQaFLGREGSGFPsRLCTPGEMVKFLT 578

iiIWiASAlHAAVNFGQYpYgYipNRpttsRrPmPeegpvDtaeyeela
iI+ +SA+HAAVN GQ ++g++ pN+P+ +R+p+P +++
46638 579 AIIFNCSAQHAAVNSGQHDFGAWMPNAPSSMRQPPPTKG----- 618

knpekallkTitsqlqalldlsvieiLSrHasDEvYLGqrdepeWtsdkk
+ + k++l+T++ + ++ 1 +++++ S+ D +LG ++ e++++
46638 619 TTTLKTYLDTLPEVNISCNNLLLFWLVSQEPKQRPGLGTYPD-EHFTEEA 667

aleAFkrFgkLaeIEkkIterNkDesLkNRvGpvklPYtLLkPs<-* (SEQ ID NO:25)
+ + F +La I I eRN + L lPYt+L P
46638 668 PRRSIAAFQSRLAQISRDIQERN--QGLA-----LPYTYLDPP 703

```

Fig. 18B

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

Alignments of top-scoring domains:

PLAT: domain 1 of 1, from 2 to 116: score 95.3, E = 1.2e-24

```

*->vsyqlivatgddstfagtgtgkvgislyGekgeskkikllkgelknlp
      + y+l v+tg      agt + +++ l+G+ ges+k+ l+++++
46638      2      AVYRLCVTTGP-YLRAGTLDNISVTLVGTCGESPKQRLDRMGR---- 43

      tlgfpggstfsfcdvdedfGelgavkiknehhslnsnptddewflksit
      +f+pgs+ ++++ + ++Gel+++++++e + + +++d w+++++i
46638      44 --DFAPGSVQKYKVRCTAELGELLRLRVHKERYAF---FRKDSWYCSRIC 88

      vedpqtqgevhFpcnsWvygktpkeylslic<-* (SEQ ID NO:26)
      v+ p++ + hFpc++W++g      ++++ lr++
46638      89 VTEPDG-SVSHFPCYQWIEG---YCTVELRPG      116
  
```

Fig. 19A

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

Alignments of top-scoring domains:

LH2_4: domain 1 of 1, from 2 to 116: score 80.9, E = 2.7e-20

*->akykvtVtlgkknvldfagttalgsllDgltldllGrqsvslsLiGae

46638 2 a+y+ +Vt+g agt + ++s+ L+G+
AVYRLCVTTG---PYLRAGTLD-----NISVTLVGTC 30

gddntgrgkesklaylerplTtlpslfargstye fefdvdedfGelgavk

46638 31 +es ++ l r++ ++fa+gs++ + + + +Gel+ +
-----GESPKQRLDRMG----RDFAPGSVQKYKVRCTAELGELLRLR 68

iknehylfwssprhsefLksitlkdLgptggkvhFpCnswVypk kkp g

46638 69 +++e+y++f r++ +++++i + + +g++ hFpC++W+ ++
VHKERYAFF----RKDSWYCSRICVTEP--DGSVSHFPCYQWIEGY---- 108

ykgkriFfan<-* (SEQ ID NO:27)

46638 109 + ++++++
--CTVELRPG 116

Fig. 19B

Applicant: Rachel E. Meyers, et al.

Title: NOVE HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

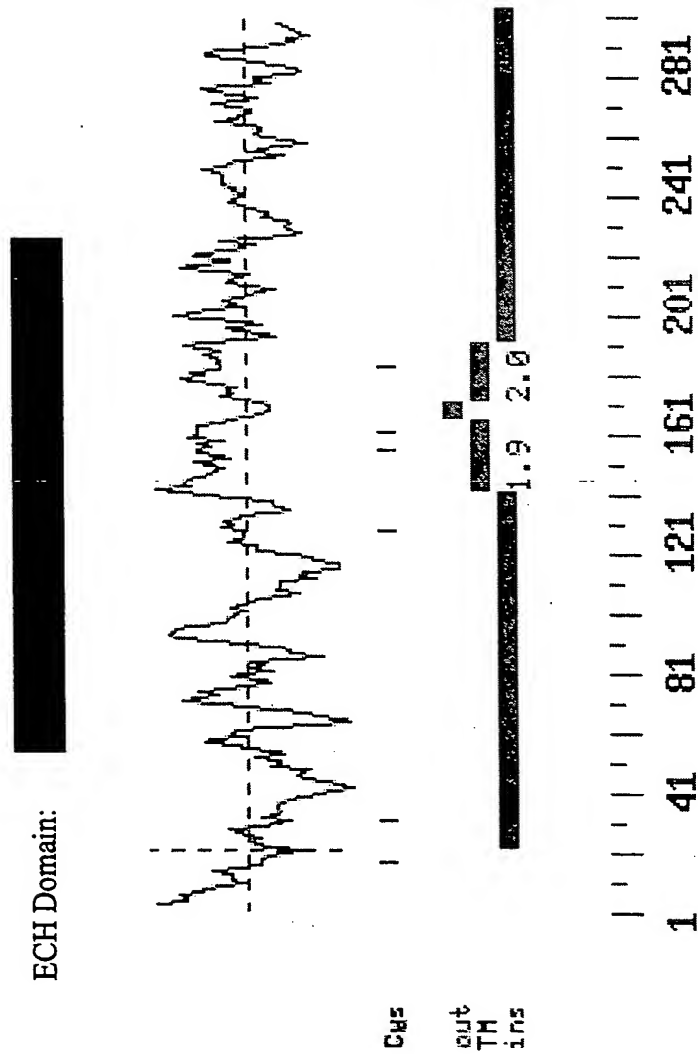


Fig. 20

Applicant: Rachel E. Meyers, et al.

Title: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF

Attorney/Agent: Janice M. Klunder

Docket No.: MPI02-107CN1M

ECH: domain 1 of 1, from 57 to 225: score 143.2, E = 4.6e-39

```

*->avikldrPeeavNalsaelItEl.ieAlekleqDpsvraVltGagp
      i+l +P+ + N+ls ++l +l+++ + ++++++++ + +
50090      57      RNIVLSNPK-KRNTLSLAMLKSLqSDILHDADSN-DLKVIIISAE-G 100

      gaFsaGaDikemaagfkeplaeqaqfsleaqdlwskledlpkPViAAVNG
      +Fs+G D+ke+++ + + a+ ++ ++ ++++++ p+PViA+VNG
50090      101 PVFSSGHDLKELTE--EQGRDYHAEVFQTCskVMMHIRNHPVPVIAMVNG 148

      yAlGGlelAlaLacDyrIAadnAkyvfglpEvklGiiPGaGGtqrLpRivG
      A ++G+ l+ +c +++A+d+++ f++p+v++G++ + + L+R+v+
50090      149 LATAAGCQLVASCNIaVAsDKSS--FATPGVNVGLFC-STPGVALARAVP 195

      vsaAlemiltGrriRAqEAkmGlVdkVVp<-* (SEQ ID NO:31)
      ++ Alem+ tG++i+AqEAl +Gl +kVVp
50090      196 RKVALEMLFTGEPIsAQEALLHGLLSKVVP 225

```

Fig. 21